Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1 Claim 1 (currently amended): A method for identifying a
2 transcribed region of interest of a genome comprising:
3
4   a) Hybridizing a plurality of nucleic acid probes with
5 a nucleic acid sample, wherein said nucleic acid sample
6 comprises transcripts from said genome, wherein said probes
7 are targeting an area of said genome; and
8
9   b) Identifying said transcribed region as a region of
10 said genome where the hybridization intensities of all
11 consecutive probes targeting said region are above a
12 threshold value.

1 Claim 2 (original): The method of claim 1 wherein said
2 probes are oligonucleotides.

1 Claim 3 (currently amended): The method of ~~claim 3~~ claim 2
2 wherein said oligonucleotides are immobilized on a
3 substrate.

1 Claim 4 (original): The method of claim 1 wherein said
2 threshold is non-specific binding.

.1 Claim 5 (previously presented): The method of claim 1
2   wherein said non-specific binding is measured using a probe
·3 containing at least one mismatched base.

1   Claim 6 (currently amended): The method of claim 1 further
2   comprising:
3
4   c)   Identifying a sub-region wherein said hybridization
5   intensities of said probes targeting said sub-region is are
6   similar, thereby indicating said sub-region as said
7   transcribed region.

1   Claim 7 (original): The method of claim 6 wherein said
2   genome is from a prokaryote.

1   Claim 8 (original): The method of claim 7 wherein said
2   transcribed region is an operon.

1   Claim 9 (previously presented): The method of claim 7
2   wherein said prokaryote is bacteria.

Claims 10-14 (canceled)